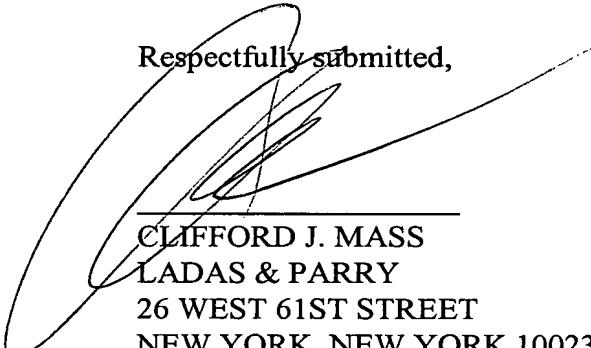


REMARKS

The above amendatory action is taken in response to the Official Communication dated April 9, 2004. The Sequence Listing has been revised to correct the errors noted in the communication. Applicants submit herewith a paper copy and a computer readable form copy of the Sequence Listing and statements that the contents of the paper and computer readable form copies are the same and include no new matter.

Applicants have now complied with the requirements in the aforementioned Official Communication and respectfully request an early examination of this application on the merits.

Respectfully submitted,



CLIFFORD J. MASS
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Oon, Chong Jin
Lim, Gek Keow
Zhao, Yi
Chen, Wei Ning

(ii) TITLE OF INVENTION: A MUTANT HUMAN HEPATITIS B VIRAL STRAIN AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Ladas & Parry
(B) STREET: 26 West 61 Street
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10023

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/719,528
(B) FILING DATE: 19-DEC-2000
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/SG98/00046
(B) FILING DATE: 19-JAN-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mass, Clifford J.
(B) REGISTRATION NUMBER: 30,086
(C) REFERENCE/DOCKET NUMBER: U-014987-0

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 708-1800

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3215 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: circular

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCCACAACA	TTCCACCAAG	CTCTGCTAGA	TCCCAGGGTG	AGGGGCCTAT	ATTTCCCTGC	60	
TGGTGGCTCC	AGTTCCGGAA	CAGTAAACCC	TGTTCCGACT	ACTGCCTCTC	CCATATCGTC	120	
AATCTTCTCG	AGGACTGGGG	ACCCCTGCACC	GAACATGGAG	AACACAACAT	CAGGATTCC	180	
AGGACCCCTG	CTCGTGTAC	AGGCGGGGTT	TTTCTCGTTG	ACAAGAATCC	TCACAATACC	240	
GCAGAGTCTA	GACTCTGGTG	GACTTCTCTC	AATTTCTAG	GGGGAGCACC	CACGTGTTCC	300	
TGGCCAAAAT	TCGCAGTCCC	CAACCTCCAA	TCACTCACCA	ACCTCTGTC	CTCCAATTG	360	
TCCTGGCTAT	CGCTGGATGT	GTCTGCGGCG	TTTTATCATA	TTCCTCTTCA	TCCTGCTGCT	420	
ATGCCTCATC	TTCTTGTG	TTCTTCTGGA	CTACCAAGGT	ATGTTGCCCG	TTTGTCCCTCT	480	
ACTTCCAGGA	ACATCAACCA	CCAGCACGGG	GCCATGCAAG	ACCTGCACGA	CTCCTGCTCA	540	
AGGAAACTCT	ACGTTCCCT	CTTGTGCTG	TACAAAACCT	TCGGACGGAA	ACTGCACTTG	600	
TATTCCCATC	CCATCATCCT	GGGCTTTCGC	AAGATTCTA	TGGGAGTGGG	CCTCAGTCCG	660	
TTTCTCCTGG	CTCAGTTTAC	TAGTGCCATT	TGTTCACTGG	TTCGTAGGGC	TTTCCCCCAC	720	
TGTTGGCTT	TCAGTTATAT	GGATGATGTG	GTATTGGGG	CGAAGTCTGT	ACAACATCTT	780	
GAGTCCCTTT	TTACCTCTAT	TACCAATT	CTTTGTCTT	TGGGTATAACA	TTAAACCCCT	840	
AATAAAACCA	AACGTTGGGG	CTACTCCCTT	AACTTCATGG	GATATGTAAT	TGGAAGTTGG	900	
GGTACTTTAC	CGCAGGAACA	TATTGTA	AAACTCAAGC	AATGTTTCG	AAAACGTCC	960	
GTAAATAGAC	CTATTGATTG	GAAAGTATGT	CAAAGAATTG	TGGGTCTTT	GGGCTTGCT	1020	
GCCCCTTTA	CACAATGTGG	CTATCCTGCC	TTGATGCCTT	TATATGCATG	TATACAATCT	1080	
AAGCAGGCTT	TCACCTTCTC	GCCAACCTAC	AAGGCCCTTC	TGTGTAAACA	ATATCTGAAC	1140	
CTTTACCCCG	TTGCCCGCA	ACGGTCCGGT	CTCTGCCAAG	TGTTGCTGA	CGCAACCCCC	1200	
ACTGGATGGG	GCTTGGCCAT	AGGCCATCAG	CGCATGGCTG	GAACCTTCT	GGCTCCTCTG	1260	
CCGATCCATA	CTGCGGA	ACT CCTAGCAGCT	TGTTTGCTC	GCAGCCGGTC	TGGAGCAAAA	1320	
CTTATCGGAA	CCGACAAC	TC TGTGCTC	TCTCGAAAT	ACACCTCC	TCCATGGCTG	1380	
CTAGGGTGTG	CTGCCAACTG	GATCCTGCC	GGGACGTCT	TTGTCTACGT	CCCCTCGGCG	1440	
CTGAATCCCG	CGGACGACCC	GTCTCGGGC	CGTTGGGC	TCTACCGTCC	CCTCTTCAT	1500	
CTGCCGTTCC	GGCCGACCAC	GGGGCGCACC	TCTCTTACG	CGGTCTCCCC	GTATGTGCCT	1560	
TCTCATCTGC	CGGACCGTGT	GCACTTCGCT	TCACCTCTGC	ACGTGCGATG	GAGACCACCG	1620	
TGAACGCACG	CCAGGTCTTG	CCCAAGGTCT	TATATAAGAG	GACTCTTGG	CTCTCAGCAA	1680	
TGTCAACGAC	CGACCTTGAG	GCATACTTCA	AAGACTGTGT	GT	TTAAAGAC	TGGGAGGAGT	1740

TGGGGGAGGA GATTAGGTTA AAGATTTATG TACTAGGAGG CTGTAGGCAT AAATTGGTCT	1800
GTTCAACCAGC ACCATGCAAC TTTTTCTCCT CTGCCTAATC ATCTCATGTT CATGTCCTAC	1860
TGTTCAAGCC TCCAAGCTGT GCCTTGGGTG GCTTTGGAC ATGGACATTG ACCCGTATAA	1920
AGAATTTGGA GCATCTGCTG AGTTACTCTC TTTTTGCCT TCTGACTTCT TTCCGTCTAT	1980
TCGAGATCTC CTCGACACCG CCTCTGCTCT GTATCAGGAG GCCTTAGAGT CTCCGAAACA	2040
TTGTTGCCT CACCATACAG CACTCAGGCA AGCTATTTG TGTTGGGTG AGTTGATGAA	2100
TCTGGCCACC TGGGTGGAA GTAATTTGGA AGATCCAGCA TCCAGGAAAT TAGTAGTCAG	2160
CTATGTCAAC GTTAATATGG GCCTAAAAGT CAGACAAATA TTGTGGTTTC ACATTTCTG	2220
TCTTACTTTT GGAAGAGAAA CTGTTCTTGA GTACTTGGTA TCTTTGGAG TGTGGATTG	2280
CACTCCTACC GCTTACAGAC CACCAAATGC CCCTATCTTA TCAACACTTC CGGAAACTAC	2340
TGTTGTTAGA CGACGAGGCA GGTCCCCTAG AAGAAGAACT CCCTCGCCTC GCAGACGAAG	2400
GTCTCAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGAA TCTCAACGTT AGTATTCTT	2460
GGACTCATAA GGTGGAAAC TTTACTGGC TTTATTCTTC TACTGTACCT GTCTTTAAC	2520
CCGAGTGGCA AATTCCCTCC TTTCCTCACA TTCATTACA AGAGGACATT ATTAATAGAT	2580
GTCAACAATA TGTGGCCCT CTTACAGTTA ATGAAAAAAG AAGATTTAA TTAATTATGC	2640
CTGCTAGGTT TTATCCTAAC CTTACTAAAT ATTTGCCCTT AGACAAAGGC ATTAAACCGT	2700
ATTATCCTGA ACATGCAGTT AATCATTACT TCAAAACTAG GCATTATTAA CATACTCTGT	2760
GGAAGGCTGG CATTCTATAT AAGAGAGAAA CTACACGCAG CGCCTCATT TGTGGTCAC	2820
CATATTCTTG GGAACAAGAG CTACAGCATG GGAGGTTGGT CTTCCAAACC TCGACAAGGC	2880
ATGGGGAGCA ATCTTGCTGT TCCCAATCCT CTGGGATTCT TTCCCGATCA CCAGTTGGAC	2940
CCTGCGTTG GAGCCAATC AAACAATCCA GATTGGACT TCAACCCCAA CAAGGATCAC	3000
TGGCCAGAGG CAAATCAGGT AGGAGTGGGA GCATTGGGC CAGGGTTCAC CCCACCACAC	3060
GGCGGTCTTT TGGGGGGGAG CCCTCAGGCT CAGGGCATAT TGACAAACAGT GCCAGCAGCA	3120
CCTCCTCCTG CCTCCACCAA TCGGCAGTCA GGAAGACAGC CTACTCCCCT CTCTCCACCT	3180
CTAAGAGACA GTCATCCTCA GGCCACGCAG TGGAA	3215

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 843 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Leu Ser Tyr Gln His Phe Arg Lys Leu Leu Leu Leu Asp Asp
1 5 10 15

Glu Ala Gly Pro Leu Glu Glu Glu Leu Pro Arg Leu Ala Asp Glu Gly
20 25 30

Leu Asn Arg Arg Val Ala Glu Asp Leu Asn Leu Gly Asn Leu Asn Val
35 40 45

Ser Ile Pro Trp Thr His Lys Val Gly Asn Phe Thr Gly Leu Tyr Ser
50 55 60

Ser Thr Val Pro Val Phe Asn Pro Glu Trp Gln Ile Pro Ser Phe Pro
65 70 75 80

His Ile His Leu Gln Glu Asp Ile Ile Asn Arg Cys Gln Gln Tyr Val
85 90 95

Gly Pro Leu Thr Val Asn Glu Lys Arg Arg Leu Lys Leu Ile Met Pro
100 105 110

Ala Arg Phe Tyr Pro Asn Leu Thr Lys Tyr Leu Pro Leu Asp Lys Gly
115 120 125

Ile Lys Pro Tyr Tyr Pro Glu His Ala Val Asn His Tyr Phe Lys Thr
130 135 140

Arg His Tyr Leu His Thr Leu Trp Lys Ala Gly Ile Leu Tyr Lys Arg
145 150 155 160

Glu Thr Thr Arg Ser Ala Ser Phe Cys Gly Ser Pro Tyr Ser Trp Glu
165 170 175

Gln Glu Leu Gln His Gly Arg Leu Val Phe Gln Thr Ser Thr Arg His
180 185 190

Gly Asp Glu Ser Cys Cys Ser Gln Ser Ser Gly Ile Leu Ser Arg Ser
195 200 205

Pro Val Gly Pro Cys Val Arg Ser Gln Leu Lys Gln Ser Arg Leu Gly
210 215 220

Leu Gln Pro Gln Gln Gly Ser Leu Ala Arg Gly Lys Ser Gly Arg Ser
225 230 235 240

Gly Ser Ile Arg Ala Arg Val His Pro Thr Thr Arg Arg Ser Phe Gly
245 250 255

Gly Glu Pro Ser Gly Ser Gly His Ile Asp Asn Ser Ala Ser Ser Thr
260 265 270

Ser Ser Cys Leu His Gln Ser Ala Val Arg Lys Thr Ala Tyr Ser His
 275 280 285
 Leu Ser Thr Ser Lys Arg Gln Ser Ser Ser Gly His Ala Val Glu Leu
 290 295 300
 His Asn Ile Pro Pro Ser Ser Ala Arg Ser Gln Gly Glu Gly Pro Ile
 305 310 315 320
 Phe Ser Cys Trp Trp Leu Gln Phe Arg Asn Ser Lys Pro Cys Ser Asp
 325 330 335
 Tyr Cys Leu Ser His Ile Val Asn Leu Leu Glu Asp Trp Gly Pro Cys
 340 345 350
 Thr Glu His Gly Glu His Asn Ile Arg Ile Pro Arg Thr Pro Ala Arg
 355 360 365
 Val Thr Gly Gly Val Phe Leu Val Asp Lys Asn Pro His Asn Thr Ala
 370 375 380
 Glu Ser Arg Leu Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro
 385 390 395 400
 Thr Cys Ser Trp Pro Lys Phe Ala Val Pro Asn Leu Gln Ser Leu Thr
 405 410 415
 Asn Leu Leu Ser Ser Asn Leu Ser Trp Leu Ser Leu Asp Val Ser Ala
 420 425 430
 Ala Phe Tyr His Ile Pro Leu His Pro Ala Ala Met Pro His Leu Leu
 435 440 445
 Val Gly Ser Ser Gly Leu Pro Arg Tyr Val Ala Arg Leu Ser Ser Thr
 450 455 460
 Ser Arg Asn Ile Asn His Gln His Gly Ala Met Gln Asp Leu His Asp
 465 470 475 480
 Ser Cys Ser Arg Lys Leu Tyr Val Ser Leu Leu Leu Tyr Lys Thr
 485 490 495
 Phe Gly Arg Lys Leu His Leu Tyr Ser His Pro Ile Ile Leu Gly Phe
 500 505 510
 Arg Lys Ile Pro Met Gly Val Gly Leu Ser Pro Phe Leu Leu Ala Gln
 515 520 525
 Phe Thr Ser Ala Ile Cys Ser Val Val Arg Arg Ala Phe Pro His Cys
 530 535 540
 Leu Ala Phe Ser Tyr Met Asp Asp Val Val Leu Gly Ala Lys Ser Val
 545 550 555 560
 Gln His Leu Glu Ser Leu Phe Thr Ser Ile Thr Asn Phe Leu Leu Ser
 565 570 575

Leu Gly Ile His Leu Asn Pro Asn Lys Thr Lys Arg Trp Gly Tyr Ser
 580 585 590
 Leu Asn Phe Met Gly Tyr Val Ile Gly Ser Trp Gly Thr Leu Pro Gln
 595 600 605
 Glu His Ile Val Leu Lys Leu Lys Gln Cys Phe Arg Lys Leu Pro Val
 610 615 620
 Asn Arg Pro Ile Asp Trp Lys Val Cys Gln Arg Ile Val Gly Leu Leu
 625 630 635 640
 Gly Phe Ala Ala Pro Phe Thr Gln Cys Gly Tyr Pro Ala Leu Met Pro
 645 650 655
 Leu Tyr Ala Cys Ile Gln Ser Lys Gln Ala Phe Thr Phe Ser Pro Thr
 660 665 670
 Tyr Lys Ala Phe Leu Cys Lys Gln Tyr Leu Asn Leu Tyr Pro Val Ala
 675 680 685
 Arg Gln Arg Ser Gly Leu Cys Gln Val Phe Ala Asp Ala Thr Pro Thr
 690 695 700
 Gly Trp Gly Leu Ala Ile Gly His Gln Arg Met Ala Gly Thr Phe Leu
 705 710 715 720
 Ala Pro Leu Pro Ile His Thr Ala Glu Leu Leu Ala Ala Cys Phe Ala
 725 730 735
 Arg Ser Arg Ser Gly Ala Lys Leu Ile Gly Thr Asp Asn Ser Val Val
 740 745 750
 Leu Ser Arg Lys Tyr Thr Ser Phe Pro Trp Leu Leu Gly Cys Ala Ala
 755 760 765
 Asn Trp Ile Leu Arg Gly Thr Ser Phe Val Tyr Val Pro Ser Ala Leu
 770 775 780
 Asn Pro Ala Asp Asp Pro Ser Arg Gly Arg Leu Gly Leu Tyr Arg Pro
 785 790 795 800
 Leu Leu His Leu Pro Phe Arg Pro Thr Thr Gly Arg Thr Ser Leu Tyr
 805 810 815
 Ala Val Ser Pro Tyr Val Pro Ser His Leu Pro Asp Arg Val His Phe
 820 825 830
 Ala Ser Pro Leu His Val Ala Trp Arg Pro Pro
 835 840

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu
1 5 10 15

Ala Val Pro Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro
20 25 30

Ala Phe Gly Ala Asn Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn
35 40 45

Lys Asp His Trp Pro Glu Ala Asn Gln Val Gly Val Gly Ala Phe Gly
50 55 60

Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu Gly Gly Ser Pro Gln
65 70 75 80

Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro Ala Ser
85 90 95

Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu
100 105 110

Arg Asp Ser His Pro Gln Ala Thr Gln Trp Asn Ser Thr Thr Phe His
115 120 125

Gln Ala Leu Leu Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly
130 135 140

Gly Ser Ser Ser Gly Thr Val Asn Pro Val Pro Thr Thr Ala Ser Pro
145 150 155 160

Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp Pro Ala Pro Asn Met Glu
165 170 175

Asn Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln Ala Gly
180 185 190

Phe Phe Ser Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser
195 200 205

Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly
210 215 220

Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro
225 230 235 240

Pro Ile Cys Pro Gly Tyr Arg Trp Asn Cys Leu Arg Arg Phe Ile Ile
245 250 255

Phe Leu Phe Ile Leu Leu Cys Leu Ile Phe Leu Leu Val Leu Leu
260 265 270

Asp	Tyr	Gln	Gly	Met	Leu	Pro	Val	Cys	Pro	Leu	Leu	Pro	Gly	Thr	Ser
275														285	
Thr	Thr	Ser	Thr	Gly	Pro	Cys	Lys	Thr	Cys	Thr	Thr	Pro	Ala	Gln	Gly
290														295	300
Asn	Ser	Thr	Phe	Pro	Ser	Cys	Cys	Cys	Thr	Lys	Pro	Ser	Asp	Gly	Asn
305														315	320
Cys	Thr	Cys	Ile	Pro	Ile	Pro	Ser	Ser	Trp	Ala	Phe	Ala	Arg	Phe	Leu
325														330	335
Trp	Glu	Trp	Ala	Ser	Val	Arg	Phe	Ser	Trp	Leu	Ser	Leu	Leu	Val	Pro
340														345	350
Phe	Val	Gln	Trp	Phe	Val	Gly	Leu	Ser	Pro	Thr	Val	Trp	Leu	Ser	Val
355														360	365
Ile	Trp	Met	Met	Trp	Tyr	Trp	Gly	Arg	Ser	Leu	Tyr	Asn	Ile	Leu	Ser
370														375	380
Pro	Phe	Leu	Pro	Leu	Leu	Pro	Ile	Phe	Phe	Cys	Leu	Trp	Val	Tyr	Ile
385														395	400

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 212 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Gln	Leu	Phe	Leu	Leu	Cys	Leu	Ile	Ile	Ser	Cys	Ser	Cys	Pro	Thr
1														15	
Val	Gln	Ala	Ser	Lys	Leu	Cys	Leu	Gly	Trp	Leu	Trp	Asp	Met	Asp	Ile
20														30	
Asp	Pro	Tyr	Lys	Glu	Phe	Gly	Ala	Ser	Ala	Glu	Leu	Leu	Ser	Phe	Leu
35														45	
Pro	Ser	Asp	Phe	Phe	Pro	Ser	Ile	Arg	Asp	Leu	Leu	Asp	Thr	Ala	Ser
50														60	
Ala	Leu	Tyr	Arg	Glu	Ala	Leu	Glu	Ser	Pro	Glu	His	Cys	Ser	Pro	His
65														75	80
His	Thr	Ala	Leu	Arg	Gln	Ala	Ile	Leu	Cys	Trp	Gly	Glu	Leu	Met	Asn
85														95	
Leu	Ala	Thr	Trp	Val	Gly	Ser	Asn	Leu	Glu	Asp	Pro	Ala	Ser	Arg	Glu
100														105	110

Leu Val Val Ser Tyr Val Asn Val Asn Met Gly Leu Lys Leu Arg Gln
 115 120 125
 Ile Leu Trp Phe His Ile Ser Cys Leu Thr Phe Gly Arg Glu Thr Val
 130 135 140
 Leu Glu Tyr Leu Val Ser Phe Gly Val Trp Ile Arg Thr Pro Thr Ala
 145 150 155 160
 Tyr Arg Pro Pro Asn Ala Pro Ile Leu Ser Thr Leu Pro Glu Thr Thr
 165 170 175
 Val Val Arg Arg Gly Arg Ser Pro Arg Arg Arg Thr Pro Ser Pro
 180 185 190
 Arg Arg Arg Arg Ser Gln Ser Pro Arg Arg Arg Ser Gln Ser Arg
 195 200 205
 Glu Ser Gln Arg
 210

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 154 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Ala Ala Arg Val Cys Cys Gln Leu Asp Pro Ala Arg Asp Val Leu
 1 5 10 15
 Cys Leu Arg Pro Val Gly Ala Glu Ser Arg Gly Arg Pro Val Ser Gly
 20 25 30
 Pro Phe Gly Ala Leu Pro Ser Pro Ser Ser Ala Val Pro Ala Asp
 35 40 45
 His Gly Ala His Leu Ser Leu Arg Gly Leu Pro Val Cys Ala Phe Ser
 50 55 60
 Ser Ala Gly Pro Cys Ala Leu Arg Phe Thr Ser Ala Arg Arg Met Glu
 65 70 75 80
 Thr Thr Val Asn Ala Arg Gln Val Leu Pro Lys Val Leu Tyr Lys Arg
 85 90 95
 Thr Leu Gly Leu Ser Ala Met Ser Thr Thr Asp Leu Glu Ala Tyr Phe
 100 105 110
 Lys Asp Cys Val Phe Lys Asp Trp Glu Glu Leu Gly Glu Glu Ile Arg
 115 120 125

Leu Lys Ile Tyr Val Leu Gly Gly Cys Arg His Lys Leu Val Cys Ser
130 135 140
Pro Ala Pro Cys Asn Phe Phe Ser Ser Ala
145 150

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA

36

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAGTCTAGAC TCTGCGGTAT TGTGA

25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GAGTCTAGAC TCGTGGTGGA CTTCT

25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TGAGAATTCT CACGGTGGTC TCCATGCGAC GT

32

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTTGTTTACG TCCCGT

16

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATAAGCTTAT GCCCCTATCT TATCAACACT TCCGGA

36